



SEQUENCE LISTING

7

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Bertilsson, Göran
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<120> SCREENING METHODS

<130> 13425-040001

<140> 09/896,791

<141> 2001-06-29

<150> 60/217,570

<151> 2000-07-12

<150> SE 0002551-0

<151> 2000-07-06

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 460

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (1)...(460)

<223> n = A,T,C or G

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cgggaccgcc	cgcagccggc	gcacgaggag	acggaggtgc	tgtaccagct	ggcgcacact	120
ctgccctttg	cgcgcggcgt	cacaccntnc	tggacaaggc	ctccatcatg	cgcctcacia	180
tcagctacct	gcgcatgacc	gcctctgcgc	acagantgga	aaaaggggga	gagccactgg	240
acgcctgcta	cctgaaggcc	ctggaggggt	tcgtcatggt	actcaccgcc	gagggagaca	300
tggcttacct	gtcggaaaaat	gtcagcaagc	acctgggcct	cagtcagtgg	acctctgttc	360
ctcctccctg	atacataacc	ccactcctgg	taccaatttc	tctctggagc	tcattggaca	420
cagtatcttt	gattttatca	tccctgtgac	caagaggaac			460

<210> 2

<211> 1100

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (19)...(939)

<400> 2

gaattcggca cgagggcc atg gcg ttg ggg ctg cag cgc gtg agg tcg aac	51
Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn	
1 5 10	
acc gag ctg cgg aag gag aag tcg cgg gac gcg gcc cgc agc cgg cgc	99
Thr Glu Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg	
15 20 25	
agc cag gag acg gag gtg ctg tac cag ctg gcg cac act ctg ccc ttt	147
Ser Gln Glu Thr Glu Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe	
30 35 40	
gcg cgc ggc gtc agc gcg cac ctg gac aag gcc tcc atc atg cgc ctc	195
Ala Arg Gly Val Ser Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu	
45 50 55	
aca atc agc tac ctg cgc atg cac cgc ctc tgc gca gca ggt gga aaa	243
Thr Ile Ser Tyr Leu Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys	
60 65 70 75	
agg ggg aga gcc act gga cgc ctg cta cct gaa ggc cct gga ggg ttt	291
Arg Gly Arg Ala Thr Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe	
80 85 90	
cgt cat ggt act cac cgc cga ggg aga cat ggc tta cct gtc gga aaa	339
Arg His Gly Thr His Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys	
95 100 105	
tgt cag caa gca cct ggg cct cag tca gtg gac ctc tgt tcc tcc tcc	387
Cys Gln Gln Ala Pro Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser	
110 115 120	
ctg ata cat aac ccc act cct ggt acc aat ttc tct ctg gag ctc att	435
Leu Ile His Asn Pro Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile	
125 130 135	
gga cac agt atc ttt gat ttt atc cat ccc tgt gac caa gag gaa ctt	483
Gly His Ser Ile Phe Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu	
140 145 150 155	
caa gac gcc ctg acc ccc agg ccg aac ctg tca aag aag aag ctg gaa	531
Gln Asp Ala Leu Thr Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu	
160 165 170	
gcc cca aca gag cgc cac ttt tcc ctg cga atg aag agc acg ctc acc	579
Ala Pro Thr Glu Arg His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr	
175 180 185	
agc aga ggg cgc acg ctc aac ctc aaa gcg gcc acc tgg aag gtg ctg	627
Ser Arg Gly Arg Thr Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu	
190 195 200	
cac tgc tca gga cat atg agg gcc tac aag ccc cct gca cag act tcc	675
His Cys Ser Gly His Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser	
205 210 215	
cct gcc ggg agc cct cgc tcc gag cct ccc ctg caa tgc ctg gtg ctt	723

Pro Ala Gly Ser Pro Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu
220 225 230 235

atc tgt gaa gcc atc ccc cag ctc ccc ttc cac gat ggt gct act ctg 771
Ile Cys Glu Ala Ile Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu
240 245 250

ggt ctt cca cag gag aag act ccc atc tct acc tta ttc acc cct ctt 819
Gly Leu Pro Gln Glu Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu
255 260 265

tgg aag gca cta ctt tgt ctt gtc aag agg tgg cct gtt cag gtg cta 867
Trp Lys Ala Leu Leu Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu
270 275 280

cag ggg aaa ggg act gaa tcc tct ctc ccc tca tgg gtg ttg tgg gcc 915
Gln Gly Lys Gly Thr Glu Ser Ser Leu Pro Ser Trp Val Leu Trp Ala
285 290 295

ctt aac cgg aaa aat tgt cct ggc taggagggag tgaaggacat ggcccagcta 969
Leu Asn Arg Lys Asn Cys Pro Gly
300 305

tccttagccc agaaacccac aaatgtctcc aaaaccacca taaagacctc tccttggttag 1029
gcaccagaga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1089
catgcggccg c 1100

<210> 3

<211> 307

<212> PRT

<213> Mus musculus

<400> 3

Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn Thr Glu Leu Arg Lys
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Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu
20 25 30
Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser
35 40 45
Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu
50 55 60
Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys Arg Gly Arg Ala Thr
65 70 75 80
Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe Arg His Gly Thr His
85 90 95
Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys Cys Gln Gln Ala Pro
100 105 110
Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser Leu Ile His Asn Pro
115 120 125
Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile Gly His Ser Ile Phe
130 135 140
Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr
145 150 155 160
Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu Ala Pro Thr Glu Arg
165 170 175
His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr
180 185 190

